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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/459,573

DATE: 04/17/2001

TIME: 11:24:37

Input Set : A:\00101066.txt

Output Set: N:\CRF3\04172001\I459573.raw

ENTERED

3 <110> APPLICANT: LIVSHITS, VITALIY  
4 ZAKATAEVA, NATALIA  
5 NAKANISHI, KAZUO  
6 VENIAMINOVICH, VLADIMIR  
7 TROSHIN, PETR  
8 TOKHMAKOVA, IRINA  
10 <120> TITLE OF INVENTION: METHOD FOR PRODUCING L-AMINO ACIDS  
12 <130> FILE REFERENCE: 0010-1066-0  
14 <140> CURRENT APPLICATION NUMBER: 09/459,573  
15 <141> CURRENT FILING DATE: 1999-12-13  
17 <150> PRIOR APPLICATION NUMBER: RU98124016  
18 <151> PRIOR FILING DATE: 1998-12-30  
20 <150> PRIOR APPLICATION NUMBER: RU99104431  
21 <151> PRIOR FILING DATE: 1999-03-09  
23 <160> NUMBER OF SEQ ID NOS: 24  
25 <170> SOFTWARE: PatentIn version 3.0  
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33 <221> NAME/KEY: misc\_feature  
34 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA  
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69 <210> SEQ ID NO: 4  
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72 <213> ORGANISM: Artificial Sequence

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144 <220> FEATURE:
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146 <222> LOCATION: (1)..(672)
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151 1          5          10          15
153 ttg cat gcc gtt tac ctg acc gta gga ctg ttc gtg att act ttt ttt      96
154 Leu His Ala Val Tyr Leu Thr Val Gly Leu Phe Val Ile Thr Phe Phe
155          20          25          30
157 aat ccg gga gcc aat ctc ttt gtg gta gta caa acc agc ctg gct tcc      144
158 Asn Pro Gly Ala Asn Leu Phe Val Val Val Gln Thr Ser Leu Ala Ser
159          35          40          45
161 ggt cga cgc gca ggg gtg ctg acc ggg ctg ggc gtg gcg ctg ggc gat      192
162 Gly Arg Arg Ala Gly Val Leu Thr Gly Leu Gly Val Ala Leu Gly Asp
163          50          55          60
165 gca ttt tat tcc ggg ttg ggt ttg ttt ggt ctt gca acg cta att acg      240
166 Ala Phe Tyr Ser Gly Leu Gly Leu Phe Gly Leu Ala Thr Leu Ile Thr
167 65          70          75          80
169 cag tgt gag gag att ttt tcg ctt atc aga atc gtc ggc ggc gct tat      288
170 Gln Cys Glu Glu Ile Phe Ser Leu Ile Arg Ile Val Gly Gly Ala Tyr
171          85          90          95
173 ctc tta tgg ttt gcg tgg tgc agc atg cgc cgc cag tca aca ccg caa      336
174 Leu Leu Trp Phe Ala Trp Cys Ser Met Arg Arg Gln Ser Thr Pro Gln
175          100          105          110
177 atg agc aca cta caa caa ccg att agc gcc ccc tgg tat gtc ttt ttt      384
178 Met Ser Thr Leu Gln Gln Pro Ile Ser Ala Pro Trp Tyr Val Phe Phe
179          115          120          125
181 cgc cgc gga tta att acc gat ctc tct aac ccg caa acc gtt tta ttt      432
182 Arg Arg Gly Leu Ile Thr Asp Leu Ser Asn Pro Gln Thr Val Leu Phe
183          130          135          140
185 ttt atc agt att ttc tca gta aca tta aat gcc gaa aca cca aca tgg      480
186 Phe Ile Ser Ile Phe Ser Val Thr Leu Asn Ala Glu Thr Pro Thr Trp
187 145          150          155          160
189 gca cgt tta atg gcc tgg gcg ggg att gtg ctc gca tca att atc tgg      528
190 Ala Arg Leu Met Ala Trp Ala Gly Ile Val Leu Ala Ser Ile Ile Trp
191          165          170          175
193 cga gtt ttt ctt agt cag gcg ttt tct ttg ccc gct gtg cgt cgt gct      576
194 Arg Val Phe Leu Ser Gln Ala Phe Ser Leu Pro Ala Val Arg Arg Ala
195          180          185          190
197 tat ggg cgt atg caa cgc gtt gcc agt cgg gtt att ggt gca att att      624
198 Tyr Gly Arg Met Gln Arg Val Ala Ser Arg Val Ile Gly Ala Ile Ile
199          195          200          205
201 ggt gta ttc gcg cta cgc ctg att tac gaa ggg gtg acg cag cgg tga      672
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207 <211> LENGTH: 223
208 <212> TYPE: PRT
209 <213> ORGANISM: Escherichia coli
211 <400> SEQUENCE: 10
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214 1          5          10          15

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217 Leu His Ala Val Tyr Leu Thr Val Gly Leu Phe Val Ile Thr Phe Phe
218                20                25                30
221 Asn Pro Gly Ala Asn Leu Phe Val Val Val Gln Thr Ser Leu Ala Ser
222                35                40                45
225 Gly Arg Arg Ala Gly Val Leu Thr Gly Leu Gly Val Ala Leu Gly Asp
226                50                55                60
229 Ala Phe Tyr Ser Gly Leu Gly Leu Phe Gly Leu Ala Thr Leu Ile Thr
230 65                70                75                80
233 Gln Cys Glu Glu Ile Phe Ser Leu Ile Arg Ile Val Gly Gly Ala Tyr
234                85                90                95
237 Leu Leu Trp Phe Ala Trp Cys Ser Met Arg Arg Gln Ser Thr Pro Gln
238                100               105               110
241 Met Ser Thr Leu Gln Gln Pro Ile Ser Ala Pro Trp Tyr Val Phe Phe
242                115               120               125
245 Arg Arg Gly Leu Ile Thr Asp Leu Ser Asn Pro Gln Thr Val Leu Phe
246                130               135               140
249 Phe Ile Ser Ile Phe Ser Val Thr Leu Asn Ala Glu Thr Pro Thr Trp
250 145               150               155               160
253 Ala Arg Leu Met Ala Trp Ala Gly Ile Val Leu Ala Ser Ile Ile Trp
254                165               170               175
257 Arg Val Phe Leu Ser Gln Ala Phe Ser Leu Pro Ala Val Arg Arg Ala
258                180               185               190
261 Tyr Gly Arg Met Gln Arg Val Ala Ser Arg Val Ile Gly Ala Ile Ile
262                195               200               205
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266                210               215               220
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270 <211> LENGTH: 639
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275 <221> NAME/KEY: CDS
276 <222> LOCATION: (1)..(639)
278 <400> SEQUENCE: 11
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281 1                5                10                15
283 gcc att ttt att gtg ttg gtg cca ggg cca aat acc ctg ttt gta ctc      96
284 Ala Ile Phe Ile Val Leu Val Pro Gly Pro Asn Thr Leu Phe Val Leu
285                20                25                30
287 aaa aat agc gtc agt agc ggt atg aaa ggc ggt tat ctt gcg gcc tgc      144
288 Lys Asn Ser Val Ser Ser Gly Met Lys Gly Gly Tyr Leu Ala Ala Cys
289                35                40                45
291 ggt gta ttt att ggc gat gcg gta ttg atg ttt ctg gca tgg gct gga      192
292 Gly Val Phe Ile Gly Asp Ala Val Leu Met Phe Leu Ala Trp Ala Gly
293                50                55                60
295 gtg gcg aca tta att aag acc acc ccg ata tta ttc aac att gta cgt      240
296 Val Ala Thr Leu Ile Lys Thr Thr Pro Ile Leu Phe Asn Ile Val Arg
297 65                70                75                80

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299 tat ctt ggt gcg ttt tat ttg ctc tat ctg ggg agt aaa att ctt tac      288
300 Tyr Leu Gly Ala Phe Tyr Leu Leu Tyr Leu Gly Ser Lys Ile Leu Tyr
301      85      90      95
303 gcg acc ctg aag ggt aaa aat agc gag gcc aaa tcc gat gag ccc caa      336
304 Ala Thr Leu Lys Gly Lys Asn Ser Glu Ala Lys Ser Asp Glu Pro Gln
305      100      105      110
307 tac ggt gct att ttt aaa cgc gcg tta att ttg agc ctg act aat ccg      384
308 Tyr Gly Ala Ile Phe Lys Arg Ala Leu Ile Leu Ser Leu Thr Asn Pro
309      115      120      125
311 aaa gcc att ttg ttc tat gtg tcg ttt ttc gta cag ttt atc gat gtt      432
312 Lys Ala Ile Leu Phe Tyr Val Ser Phe Phe Val Gln Phe Ile Asp Val
313      130      135      140
315 aat gcc cca cat acg gga att tca ttc ttt att ctg gcg gcg acg ctg      480
316 Asn Ala Pro His Thr Gly Ile Ser Phe Phe Ile Leu Ala Ala Thr Leu
317 145      150      155      160
319 gaa ctg gtg agt ttc tgc tat ttg agc ttc ctg att ata tct ggt gct      528
320 Glu Leu Val Ser Phe Cys Tyr Leu Ser Phe Leu Ile Ile Ser Gly Ala
321      165      170      175
323 ttt gtc acg cag tac ata cgt acc aaa aag aaa ctg gct aaa gtt ggc      576
324 Phe Val Thr Gln Tyr Ile Arg Thr Lys Lys Lys Leu Ala Lys Val Gly
325      180      185      190
327 aac tca ctg att ggt ttg atg ttc gtg ggt ttc gct gcc cga ctg gcg      624
328 Asn Ser Leu Ile Gly Leu Met Phe Val Gly Phe Ala Ala Arg Leu Ala
329      195      200      205
331 acg ctg caa tcc tga /      639
332 Thr Leu Gln Ser
333      210
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337 <211> LENGTH: 212
338 <212> TYPE: PRT
339 <213> ORGANISM: Escherichia coli
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348      20      25      30
351 Lys Asn Ser Val Ser Ser Gly Met Lys Gly Gly Tyr Leu Ala Ala Cys
352      35      40      45
355 Gly Val Phe Ile Gly Asp Ala Val Leu Met Phe Leu Ala Trp Ala Gly
356      50      55      60
359 Val Ala Thr Leu Ile Lys Thr Thr Pro Ile Leu Phe Asn Ile Val Arg
360 65      70      75      80
363 Tyr Leu Gly Ala Phe Tyr Leu Leu Tyr Leu Gly Ser Lys Ile Leu Tyr
364      85      90      95
367 Ala Thr Leu Lys Gly Lys Asn Ser Glu Ala Lys Ser Asp Glu Pro Gln
368      100      105      110
371 Tyr Gly Ala Ile Phe Lys Arg Ala Leu Ile Leu Ser Leu Thr Asn Pro
372      115      120      125
375 Lys Ala Ile Leu Phe Tyr Val Ser Phe Phe Val Gln Phe Ile Asp Val

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VERIFICATION SUMMARY

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